

WHAT IS CLAIMED IS:

1. An isolated or recombinant polynucleotide comprising:

(a) a nucleotide sequence encoding an amino acid sequence that can be optimally aligned with a sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457 to generate a similarity score of at least 430, using the BLOSUM62 matrix, a gap existence penalty of 11, and a gap extension penalty of 1; or

(b) a complementary nucleotide sequence thereof.

2. The isolated or recombinant polynucleotide of claim 1, wherein the polypeptide has glyphosate N-acetyl transferase activity.

3. The isolated or recombinant polynucleotide of claim 2, wherein the polypeptide catalyzes the acetylation of glyphosate with a k_{cat}/K_m of at least $10 \text{ mM}^{-1} \text{ min}^{-1}$ for glyphosate.

4. The isolated or recombinant polynucleotide of claim 2, wherein the polypeptide catalyzes the acetylation of aminomethylphosphonic acid.

5. An isolated or recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide having glyphosate N-acetyltransferase activity, the polypeptide comprising an amino acid sequence comprising at least 20 contiguous amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457.

6. The isolated or recombinant polynucleotide of claim 5, wherein the polypeptide comprises an amino acid sequence comprising at least 50 contiguous amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457.

7. The isolated or recombinant polynucleotide of claim 5, wherein the polypeptide comprises an amino acid sequence comprising at least 100 contiguous amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457.

8. The isolated or recombinant polynucleotide of claim 5, wherein the polypeptide comprises an amino acid sequence comprising about 140 contiguous amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457.

9. The isolated or recombinant polynucleotide of claim 5, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457.

10. The isolated or recombinant polynucleotide of claim 5, comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:193 and SEQ ID NO:205.

11. The polynucleotide of claim 1, wherein a parental codon has been replaced by a synonymous codon that is preferentially used in plants relative to the parental codon.

12. The polynucleotide of claim 1, further comprising a nucleotide sequence encoding an N-terminal chloroplast transit peptide.

13. A non-native variant of the polynucleotide of claim 1, wherein one or more amino acids of the encoded polypeptide have been mutated.

14. A nucleic acid construct comprising the polynucleotide of claim 1.

15. The nucleic acid construct of claim 14, comprising a promoter operably linked to the polynucleotide of claim 1, where the promoter is heterologous with respect to the polynucleotide and effective to cause sufficient expression of the encoded polypeptide to enhance the glyphosate tolerance of a plant cell transformed with the nucleic acid construct.

16. The nucleic acid construct of claim 14, wherein the polynucleotide sequence of claim 1 functions as a selectable marker.

17. The nucleic acid construct of claim 14, wherein the construct is a vector.

18. The vector of claim 17 comprising a second polynucleotide sequence encoding a second polypeptide that confers a detectable phenotypic trait upon a cell or organism expressing the second polypeptide at an effective level.

19. The vector of claim 18, wherein the detectable phenotypic trait functions as selectable marker.

20. The vector of claim 19, wherein the detectable phenotypic trait consists of herbicide resistance, pest resistance, or a visible marker.

21. The vector of claim 17, wherein the vector comprises a T-DNA sequence.

22. The vector of claim 17, wherein the polynucleotide is operably linked to a regulatory sequence.

23. The vector of claim 17, wherein the vector is a plant transformation vector.

24. An isolated or recombinant polynucleotide comprising:

- (a) a nucleotide that hybridizes under stringent conditions over substantially the entire length of a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457;
- (b) a complementary nucleotide sequence thereof; or
- (c) a fragment of (a) or (b) that encodes a polypeptide have glyphosate N-acetyltransferase activity

25. The polynucleotide of claim 24, comprising a nucleotide sequence that encodes a glyphosate N-acetyl transferase.

26. A composition comprising two or more polynucleotides of claim 1.

27. The composition of claim 26 comprising at least ten polynucleotides of claim 1.

28. A cell comprising at least one polynucleotide of claim 1, wherein the polynucleotide is heterologous to the cell.

29. The cell of claim 28, wherein the polynucleotide is operably linked to a regulatory sequence.

30. A cell transduced by the vector of claim 17.

31. The cell of claim 28 or 30, wherein the cell is a transgenic plant cell.

32. The transgenic plant cell of claim 31, wherein the plant cell expresses an exogenous polypeptide with glyphosate N-acetyl transferase activity.

33. A transgenic plant or transgenic plant explant comprising the cell of claim 32.

34. The transgenic plant or transgenic plant explant of claim 33, wherein the plant or plant explant expresses a polypeptide with glyphosate N-acetyl transferase activity.

35. The transgenic plant or transgenic plant explant of claim 34, wherein the transgenic plant or plant explant is a crop plant selected from among the genera:

Eleusine, Lolium, Bambusa, Brassica, Dactylis, Sorghum, Pennisetum, Zea, Oryza, Triticum, Secale, Avena, Hordeum, Saccharum, Coix, Glycine and *Gossypium*.

36. The transgenic plant or transgenic plant explant of claim 34, wherein the transgenic plant or plant explant is *Arabidosis*.

37. The transgenic plant or transgenic plant explant of claim 34, wherein the transgenic plant or plant explant is *Gossypium*.

38. The transgenic plant or transgenic plant explant of claim 34, wherein the plant or plant explant exhibits enhanced resistance to glyphosate as compared to a wild
5 type plant of the same species, strain or cultivar.

39. A seed produced by the plant of claim 34.

40. A transgenic plant which contains a heterologous gene which encodes a glyphosate N-acetyltransferase having a k_{cat}/K_m of at least $10 \text{ mM}^{-1} \text{ min}^{-1}$ for glyphosate, wherein the plant exhibits tolerance to glyphosate applied at a level effective
10 to inhibit the growth of the same plant lacking the heterologous gene, without significant yield reduction due to herbicide application.

41. The transgenic plant of claim 40, wherein the glyphosate N-acetyltransferase catalyzes the acetylation of aminomethylphosphonic acid.

42. An isolated or recombinant polypeptide comprising an amino acid
15 sequence that can be optimally aligned with a sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457 to generate a similarity score of at least 430 using the BLOSUM62 matrix, a gap existence penalty of 11, and a gap extension penalty of 1, wherein the polypeptide has glyphosate N-acetyl transferase activity.

20 43. The isolated or recombinant polypeptide of claim 42, wherein the polypeptide catalyzes the acetylation of glyphosate with a k_{cat}/K_m of at least $10 \text{ mM}^{-1} \text{ min}^{-1}$ for glyphosate.

44. The isolated or recombinant polypeptide of claim 43, wherein the polypeptide catalyzes the acetylation of glyphosate with a k_{cat}/K_m of at least $100 \text{ mM}^{-1} \text{ min}^{-1}$ for glyphosate.
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45. The isolated or recombinant polypeptide of claim 44, wherein the polypeptide catalyzes the acetylation of aminomethylphosphonic acid.

46. An isolated or recombinant polypeptide having glyphosate N-acetyltransferase activity, the polypeptide comprising an amino acid sequence comprising
30 at least 20 contiguous amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:445 and SEQ ID NO:457.

47. The isolated or recombinant polypeptide of claim 46, wherein the polypeptide comprises an amino acid sequence comprising at least 50 contiguous amino

acids of an amino acid sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457.

48. The isolated or recombinant polypeptide of claim 46, wherein the polypeptide comprises an amino acid sequence comprising at least 100 contiguous amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457.

49. The isolated or recombinant polypeptide of claim 46, wherein the polypeptide comprises an amino acid sequence comprising about 140 contiguous amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457.

50. The isolated or recombinant polypeptide of claim 46, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457.

51. The polynucleotide sequence of claim 42 further comprising an N-terminal chloroplast transit peptide.

52. A non-native variant of the polypeptide of claim 42, wherein one or more amino acids of the polypeptide have been mutated.

53. A non-native variant of the polypeptide of claim 42, wherein one or more amino acids of the polypeptide have been altered relative to a parental polypeptide.

54. The polypeptide of claim 53, wherein the polypeptide is produced by a diversity generating procedure.

55. The polypeptide of claim 54, wherein the diversity generating procedures comprises mutation or recombination of at least one parental polynucleotide encoding a glyphosate N-acetyltransferase polypeptide.

56. The polypeptide of claim 55, wherein the parental polynucleotide is a polynucleotide of claim 1.

57. The polypeptide of claim 42 comprising a secretion sequence or a localization sequence.

58. The polypeptide of claim 57 comprising a chloroplast transit sequence.

59. A polypeptide which is specifically bound by a polyclonal antisera raised against one or more antigen, the antigen comprising an amino acid sequence selected from the group consisting of SEQ ID NO:300, SEQ ID NO:445 and SEQ ID NO:457.

60. A polypeptide having GAT activity characterized by:

- (a) a k_m for glyphosate of at least about 2 mM or less;
- (b) a k_m for acetyl CoA of at least about 200 μ M or less; and
- (c) a k_{cat} equal to at least about 6/minute.

5 61. A method of producing a glyphosate resistant transgenic plant or plant cell comprising:

- (a) transforming a plant or plant cell with a polynucleotide encoding a glyphosate N-acetyltransferase; and
- (b) optionally regenerating a transgenic plant from the transformed plant cell.

10 62. The method of claim 61, wherein the polynucleotide is a polynucleotide of claim 1.

63. The method of claim 61, wherein the polynucleotide is derived from a bacterial source.

15 64. The method of claim 61, comprising growing the transformed plant or plant cell in a concentration of glyphosate that inhibits the growth of a wild-type plant of the same species, which concentration does not inhibit the growth of the transformed plant.

65. The method of claim 64, comprising growing the transformed plant or plant cell or progeny of the plant or plant cell in increasing concentrations of glyphosate.

20 66. The method of claim 64, comprising growing the transformed plant or plant cell in a concentration of glyphosate that is lethal to a wild-type plant or plant cell of the same species.

67. The method of claim 62, which comprises propagating a plant transformed with the polynucleotide of claim 1.

25 68. The method of claim 67, wherein a first plant is propagated by crossing between the first plant and a second plant, such that at least some progeny of the cross display glyphosate tolerance.

69. A method for producing a variant of a polynucleotide of claim 1 comprising recursively recombining a polynucleotide of claim 1 with a second polynucleotide, thereby forming a library of variant polynucleotides.

30 70. The method of claim 69, comprising selecting a variant polynucleotide from the library on the basis of glyphosate N-acetyltransferase activity.

71. The method of claim 70, wherein the recursive recombination is performed in vitro.

72. The method of claim 70, wherein the recursive recombination is performed in vivo.

73. The method of claim 70, wherein the recursive recombination is performed in silico.

5 74. The method of claim 70, wherein the recursive recombination comprises family shuffling.

75. The method of claim 70, wherein the recursive recombination comprises a synthetic shuffling method.

10 76. The method of claim 70, comprising replacing at least one parental codon in a nucleotide sequence with a synonymous codon that is preferentially used in plants relative to the parental codon.

77. A library of variant polynucleotides produced by the method of claim 70.

78. A population of cells comprising the library of claim 77.

15 79. A recombinant polynucleotide produced by the method of claim 70, wherein the recombinant polynucleotide encodes a polypeptide with glyphosate N-acetyltransferase activity.

80. A cell comprising the polynucleotide of claim 79.

81. The cell of claim 80, wherein the cell is a plant cell.

20 82. The cell of claim 81, wherein the cell is a transgenic plant cell.

83. A seed produced by the plant of claim 82.

84. A polypeptide encoded by the polynucleotide of claim 79.

85. A method for producing a variant of a polynucleotide of claim 1 comprising mutating the polynucleotide.

25 86. A polynucleotide produced by the method of claim 85.

87. A method for selecting a plant or cell containing a nucleic acid construct, the method comprising:

(a) providing a transgenic plant or cell containing a nucleic acid construct, wherein the nucleic acid construct comprises a nucleotide sequence that encodes a glyphosate N-acetyltransferase;

30 (b) growing the plant or cell in the presence of glyphosate under conditions where the glyphosate N-acetyltransferase is expressed at an effective level, whereby the transgenic plant or cell grows at a rate that is discernibly greater than the plant or cell would grow if it did not contain the nucleic acid construct.

88. The method of claim 87, wherein the nucleic acid construct comprises a second nucleotide sequence encoding a polypeptide and a regulatory sequence operably linked to the second nucleotide sequence.

5 89. A method for selectively controlling weeds in a field containing a crop comprising:

- (a) planting the field with crop seeds or plants which are glyphosate-tolerant as a result of being transformed with a gene encoding a glyphosate N-acetyltransferase; and
- (b) applying to the crop and weeds in the field a sufficient amount of glyphosate to control the weeds without significantly affecting the crop.

10 90. A method of producing a genetically transformed plant that is tolerant toward glyphosate, comprising:

- (a) inserting into the genome of a plant cell a recombinant, double-stranded DNA molecule comprising:

- 15 (i) a promoter which functions in plant cells to cause the production of an RNA sequence;
 - (ii) a structural DNA sequence that causes the production of an RNA sequence which encodes a polypeptide of claim 42; and
 - (iii) a 3' non-translated region which functions in plant cells to cause the addition of a stretch of polyadenyl nucleotides to the 3' end of the RNA sequence;
- 20 where the promoter is heterologous with respect to the structural DNA sequence and adapted to cause sufficient expression of the encoded polypeptide to enhance the glyphosate tolerance of a plant cell transformed with the DNA molecule;

- b) obtaining a transformed plant cell; and
 - c) regenerating from the transformed plant cell a genetically transformed plant which has
- 25 increased tolerance to glyphosate.

91. A method for producing a crop comprising:

- (a) growing a crop plant that is glyphosate-tolerant as a result of being transformed with a gene encoding a glyphosate N-acetyltransferase, under conditions such that the crop plant produces a crop; and
- 30 (b) harvesting a crop from the crop plant.

92. The method of claim 91 that comprises applying glyphosate to the crop plant at a concentration effective to control weeds.

93. The method of claim 92, where the crop is cotton, corn, or soybean.

94. The isolated or recombinant polynucleotide of claim 1, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

- (a) at positions 2, 4, 15, 19, 26, 28, 31, 45, 51, 54, 86, 90, 91, 97, 103, 105, 106, 114, 123,
129, 139, and/or 145 the amino acid residue is B1; and
(b) at positions 3, 5, 8, 10, 11, 14, 17, 18, 24, 27, 32, 37, 38, 47, 48, 49, 52, 57, 58, 61, 62,
63, 68, 69, 79, 80, 82, 83, 89, 92, 100, 101, 104, 119, 120, 124, 125, 126, 128, 131,
143, and/or 144 the amino acid residue is B2;

wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y,

and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

95. The isolated or recombinant polynucleotide of claim 1, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 80% conform to the following restrictions:

- (a) at positions 2, 4, 15, 19, 26, 28, 51, 54, 86, 90, 91, 97, 103, 105, 106, 114, 129,
139, and/or 145 the amino acid residue is Z1;
(b) at positions 31 and/or 45 the amino acid residue is Z2;
(c) at positions 8 and/or 89 the amino acid residue is Z3;
(d) at positions 82, 92, 101 and/or 120 the amino acid residue is Z4;
(e) at positions 3, 11, 27 and/or 79 the amino acid residue is Z5;
(f) at position 123 the amino acid residue is Z1 or Z2;
(g) at positions 12, 33, 35, 39, 53, 59, 112, 132, 135, 140, and/or 146 the amino acid
residue is Z1 or Z3;
(h) at position 30 the amino acid residue is Z1 or Z4;
(i) at position 6 the amino acid residue is Z1 or Z6;
(j) at positions 81 and/or 113 the amino acid residue is Z2 or Z3;
(k) at positions 138 and/or 142 the amino acid residue is Z2 or Z4;
(l) at positions 5, 17, 24, 57, 61, 124 and/or 126 the amino acid residue is Z3 or Z4;
(m) at position 104 the amino acid residue is Z3 or Z5;
(n) at positions 38, 52, 62 and/or 69 the amino acid residue is Z3 or Z6;
(o) at positions 14, 119 and/or 144 the amino acid residue is Z4 or Z5;
(p) at position 18 the amino acid residue is Z4 or Z6;
(q) at positions 10, 32, 48, 63, 80 and/or 83 the amino acid residue is Z5 or Z6;
(r) at position 40 the amino acid residue is Z1, Z2 or Z3;

- (t) at positions 65 and/or 96 the amino acid residue is Z1, Z3 or Z5;
- (u) at positions 84 and/or 115 the amino acid residue is Z1, Z3 or Z4;
- (v) at position 93 the amino acid residue is Z2, Z3 or Z4;
- (w) at position 130 the amino acid residue is Z2, Z4 or Z6;

- 5 (x) at positions 47 and/or 58 the amino acid residue is Z3, Z4 or Z6;
- (y) at positions 49, 68, 100 and/or 143 the amino acid residue is Z3, Z4 or Z5;
- (z) at position 131 the amino acid residue is Z3, Z5 or Z6;
- (aa) at positions 125 and/or 128 the amino acid residue is Z4, Z5 or Z6;
- (ab) at position 67 the amino acid residue is Z1, Z3, Z4 or Z5;
- 10 (ac) at position 60 the amino acid residue is Z1, Z4, Z5 or Z6; and
- (ad) at position 37 the amino acid residue is Z3, Z4, Z5 or Z6;

wherein Z1 is an amino acid selected from the group consisting of A, I, L, M, and V; Z2 is an amino acid selected from the group consisting of F, W, and Y; Z3 is an amino acid selected from the group consisting of N, Q, S, and T; Z4 is an amino acid selected from the group consisting of R, H, and K; Z5 is an amino acid selected from the group consisting of D and E; and Z6 is an amino acid selected from the group consisting of C, G, and P.

96. The isolated or recombinant polynucleotide of claim 1, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

- (a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110, 117, 118, 121, and/or 141 the amino acid residue is B1; and
 - (b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95, 99, 102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2;
- wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y, and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

97. The isolated or recombinant polynucleotide of claim 1, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

- (a) at positions 1, 7, 9, 20, 36, 42, 50, 64, 72, 75, 76, 78, 94, 98, 110, 121, and/or 141 the amino acid residue is Z1;

(b) at positions 13, 46, 56, 70, 107, 117, and/or 118 the amino acid residue is Z2;

(c) at positions 23, 55, 71, 77, 88, and/or 109 the amino acid residue is Z3;

(d) at positions 16, 21, 41, 73, 85, 99, and/or 111 the amino acid residue is Z4;

(e) at positions 34 and/or 95 the amino acid residue is Z5;

5 (f) at position 22, 25, 29, 43, 44, 66, 74, 87, 102, 108, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is Z6;

wherein Z1 is an amino acid selected from the group consisting of A, I, L, M, and V; Z2 is an amino acid selected from the group consisting of F, W, and Y; Z3 is an amino acid selected from the group consisting of N, Q, S, and T; Z4 is an amino acid selected from the group consisting of R, H, and K; Z5 is an amino acid selected from the group consisting of D and E; and Z6 is an amino acid selected from the group consisting of C, G, and P.

98. The isolated or recombinant polynucleotide of claim 94, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

(a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110, 117,

118, 121, and/or 141 the amino acid residue is B1; and

(b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95, 99,

102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2;

wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y, and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

99. The isolated or recombinant polynucleotide of claim 94, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

(a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110, 117,

118, 121, and/or 141 the amino acid residue is B1; and

(b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95, 99,

102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2;

wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y, and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

100. The isolated or recombinant polynucleotide of claim 94, wherein of
5 the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

(a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110, 117,
118, 121, and/or 141 the amino acid residue is B1; and

10 (b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95, 99,

102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2;
wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y,

and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E,
15 G, H, K, P, S, and T.

101. The isolated or recombinant polynucleotide of claim 95, wherein of
the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

(a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110,
20 117,
118, 121, and/or 141 the amino acid residue is B1; and

(b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95,
99,

102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2;

25 wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y, and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

102. The isolated or recombinant polynucleotide of claim, wherein of the
amino acid residues in the amino acid sequence that correspond to the following positions,
30 at least 80% conform to the following restrictions:

(a) at position 2 the amino acid residue is I or L;

(b) at position 3 the amino acid residue is E or D;

(c) at position 4 the amino acid residue is V, A or I;

(d) at position 5 the amino acid residue is K, R or N;

- (e) at position 6 the amino acid residue is P or L;
 (f) at position 8 the amino acid residue is N, S or T;
 (g) at position 10 the amino acid residue is E or G;
 (h) at position 11 the amino acid residue is D or E;
- 5 (i) at position 12 the amino acid residue is T or A;
 (j) at position 14 the amino acid residue is E or K;
 (k) at position 15 the amino acid residue is I or L;
 (l) at position 17 the amino acid residue is H or Q;
 (m) at position 18 the amino acid residue is R, C or K;
- 10 (n) at position 19 the amino acid residue is I or V;
 (o) at position 24 the amino acid residue is Q or R;
 (p) at position 26 the amino acid residue is L or I;
 (q) at position 27 the amino acid residue is E or D;
 (r) at position 28 the amino acid residue is A or V;
- 15 (s) at position 30 the amino acid residue is K, M or R;
 (t) at position 31 the amino acid residue is Y or F;
 (u) at position 32 the amino acid residue is E or G;
 (v) at position 33 the amino acid residue is T, A or S;
 (w) at position 35 the amino acid residue is L, S or M;
- 20 (x) at position 37 the amino acid residue is R, G, E or Q;
 (y) at position 38 the amino acid residue is G or S;
 (z) at position 39 the amino acid residue is T, A or S;
 (aa) at position 40 the amino acid residue is F, L or S;
 (ab) at position 45 the amino acid residue is Y or F;
- 25 (ac) at position 47 the amino acid residue is R, Q or G;
 (ad) at position 48 the amino acid residue is G or D;
 (ae) at position 49 the amino acid residue is K, R, E or Q;
 (af) at position 51 the amino acid residue is I or V;
 (ag) at position 52 the amino acid residue is S, C or G;
- 30 (ah) at position 53 the amino acid residue is I or T;
 (ai) at position 54 the amino acid residue is A or V;
 (aj) at position 57 the amino acid residue is H or N;
 (ak) at position 58 the amino acid residue is Q, K, N or P;
 (al) at position 59 the amino acid residue is A or S;

- (am) at position 60 the amino acid residue is E, K, G, V or D;
 (an) at position 61 the amino acid residue is H or Q;
 (ao) at position 62 the amino acid residue is P, S or T;
 (ap) at position 63 the amino acid residue is E, G or D;
 5 (aq) at position 65 the amino acid residue is E, D, V or Q;
 (ar) at position 67 the amino acid residue is Q, E, R, L, H or K;
 (as) at position 68 the amino acid residue is K, R, E, or N;
 (at) at position 69 the amino acid residue is Q or P;
 (au) at position 79 the amino acid residue is E or D;
 10 (av) at position 80 the amino acid residue is G or E;
 (aw) at position 81 the amino acid residue is Y, N or F;
 (ax) at position 82 the amino acid residue is R or H;
 (ay) at position 83 the amino acid residue is E, G or D;
 (az) at position 84 the amino acid residue is Q, R or L;
 15 (ba) at position 86 the amino acid residue is A or V;
 (bb) at position 89 the amino acid residue is T or S;
 (bc) at position 90 the amino acid residue is L or I;
 (bd) at position 91 the amino acid residue is I or V;
 (be) at position 92 the amino acid residue is R or K;
 20 (bf) at position 93 the amino acid residue is H, Y or Q;
 (bg) at position 96 the amino acid residue is E, A or Q;
 (bh) at position 97 the amino acid residue is L or I;
 (bi) at position 100 the amino acid residue is K, R, N or E;
 (bj) at position 101 the amino acid residue is K or R;
 25 (bk) at position 103 the amino acid residue is A or V;
 (bl) at position 104 the amino acid residue is D or N;
 (bm) at position 105 the amino acid residue is L or M;
 (bn) at position 106 the amino acid residue is L or I;
 (bo) at position 112 the amino acid residue is T or I;
 30 (bp) at position 113 the amino acid residue is S, T or F;
 (bq) at position 114 the amino acid residue is A or V;
 (br) at position 115 the amino acid residue is S, R or A;
 (bs) at position 119 the amino acid residue is K, E or R;
 (bt) at position 120 the amino acid residue is K or R;

- (bu) at position 123 the amino acid residue is F or L;
- (bv) at position 124 the amino acid residue is S or R;
- (bw) at position 125 the amino acid residue is E, K, G or D;
- (bx) at position 126 the amino acid residue is Q or H;
- 5 (by) at position 128 the amino acid residue is E, G or K;
- (bz) at position 129 the amino acid residue is V, I or A;
- (ca) at position 130 the amino acid residue is Y, H, F or C;
- (cb) at position 131 the amino acid residue is D, G, N or E;
- (cc) at position 132 the amino acid residue is I, T, A, M, V or L;
- 10 (cd) at position 135 the amino acid residue is V, T, A or I;
- (ce) at position 138 the amino acid residue is H or Y;
- (cf) at position 139 the amino acid residue is I or V;
- (cg) at position 140 the amino acid residue is L or S;
- (ch) at position 142 the amino acid residue is Y or H;
- 15 (ci) at position 143 the amino acid residue is K, T or E;
- (cj) at position 144 the amino acid residue is K, E or R;
- (ck) at position 145 the amino acid residue is L or I; and
- (cl) at position 146 the amino acid residue is T or A.

103. The isolated or recombinant polynucleotide of claim 1, wherein of the
 20 amino acid residues in the amino acid sequence that correspond to the following positions,
 at least 80% conform to the following restrictions:

- (a) at position 9, 76, 94 and 110 the amino acid residue is A;
- (b) at position 29 and 108 the amino acid residue is C;
- (c) at position 34 the amino acid residue is D;
- 25 (d) at position 95 the amino acid residue is E;
- (e) at position 56 the amino acid residue is F;
- (f) at position 43, 44, 66, 74, 87, 102, 116, 122, 127 and 136 the amino acid residue is G;
- (g) at position 41 the amino acid residue is H;
- (h) at position 7 the amino acid residue is I;
- 30 (i) at position 85 the amino acid residue is K;
- (j) at position 20, 36, 42, 50, 72, 78, 98 and 121 the amino acid residue is L;
- (k) at position 1, 75 and 141 the amino acid residue is M;
- (l) at position 23, 64 and 109 the amino acid residue is N;
- (m) at position 22, 25, 133, 134 and 137 the amino acid residue is P;

- (n) at position 71 the amino acid residue is Q;
- (o) at position 16, 21, 73, 99 and 111 the amino acid residue is R;
- (p) at position 55 and 88 the amino acid residue is S;
- (q) at position 77 the amino acid residue is T;
- 5 (r) at position 107 the amino acid residue is W; and
- (s) at position 13, 46, 70, 117 and 118 the amino acid residue is Y.

104. The isolated or recombinant polynucleotide of claim 102, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

- 10 (a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110, 117, 118, 121, and/or 141 the amino acid residue is B1; and
- (b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95, 99,
- 15 102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2; wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y, and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

20 105. The isolated or recombinant polynucleotide of claim 103, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

- (a) at positions 2, 4, 15, 19, 26, 28, 31, 45, 51, 54, 86, 90, 91, 97, 103, 105, 106, 114, 123, 129, 139, and/or 145 the amino acid residue is B1; and
- (b) at positions 3, 5, 8, 10, 11, 14, 17, 18, 24, 27, 32, 37, 38, 47, 48, 49, 52, 57, 58, 61, 62,
- 25 63, 68, 69, 79, 80, 82, 83, 89, 92, 100, 101, 104, 119, 120, 124, 125, 126, 128, 131, 143, and/or 144 the amino acid residue is B2;
- wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y, and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

30 106. The isolated or recombinant polynucleotide of claim 102, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

- (a) at positions 1, 7, 9, 20, 36, 42, 50, 64, 72, 75, 76, 78, 94, 98, 110, 121, and/or 141 the amino acid residue is Z1;

- (b) at positions 13, 46, 56, 70, 107, 117, and/or 118 the amino acid residue is Z2;
- (c) at positions 23, 55, 71, 77, 88, and/or 109 the amino acid residue is Z3;
- (d) at positions 16, 21, 41, 73, 85, 99, and/or 111 the amino acid residue is Z4;
- (e) at positions 34 and/or 95 the amino acid residue is Z5;
- 5 (f) at position 22, 25, 29, 43, 44, 66, 74, 87, 102, 108, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is Z6;

wherein Z1 is an amino acid selected from the group consisting of A, I, L, M, and V; Z2 is an amino acid selected from the group consisting of F, W, and Y; Z3 is an amino acid selected from the group consisting of N, Q, S, and T; Z4 is an amino acid selected from the group consisting of R, H, and K; Z5 is an amino acid selected from the group consisting of D and E; and Z6 is an amino acid selected from the group consisting of C, G, and P.

107. The isolated or recombinant polynucleotide of claim 103, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 80% conform to the following restrictions:

- (a) at positions 2, 4, 15, 19, 26, 28, 51, 54, 86, 90, 91, 97, 103, 105, 106, 114, 129, 139, and/or 145 the amino acid residue is Z1;
- (b) at positions 31 and/or 45 the amino acid residue is Z2;
- (c) at positions 8 and/or 89 the amino acid residue is Z3;
- 20 (d) at positions 82, 92, 101 and/or 120 the amino acid residue is Z4;
- (e) at positions 3, 11, 27 and/or 79 the amino acid residue is Z5;
- (f) at position 123 the amino acid residue is Z1 or Z2;
- (g) at positions 12, 33, 35, 39, 53, 59, 112, 132, 135, 140, and/or 146 the amino acid residue is Z1 or Z3;
- 25 (h) at position 30 the amino acid residue is Z1 or Z4;
- (i) at position 6 the amino acid residue is Z1 or Z6;
- (j) at positions 81 and/or 113 the amino acid residue is Z2 or Z3;
- (k) at positions 138 and/or 142 the amino acid residue is Z2 or Z4;
- (l) at positions 5, 17, 24, 57, 61, 124 and/or 126 the amino acid residue is Z3 or Z4;
- 30 (m) at position 104 the amino acid residue is Z3 or Z5;
- (o) at positions 38, 52, 62 and/or 69 the amino acid residue is Z3 or Z6;
- (p) at positions 14, 119 and/or 144 the amino acid residue is Z4 or Z5;
- (q) at position 18 the amino acid residue is Z4 or Z6;
- (r) at positions 10, 32, 48, 63, 80 and/or 83 the amino acid residue is Z5 or Z6;

- (s) at position 40 the amino acid residue is Z1, Z2 or Z3;
- (t) at positions 65 and/or 96 the amino acid residue is Z1, Z3 or Z5;
- (u) at positions 84 and/or 115 the amino acid residue is Z1, Z3 or Z4;
- (v) at position 93 the amino acid residue is Z2, Z3 or Z4;
- 5 (w) at position 130 the amino acid residue is Z2, Z4 or Z6;
- (x) at positions 47 and/or 58 the amino acid residue is Z3, Z4 or Z6;
- (y) at positions 49, 68, 100 and/or 143 the amino acid residue is Z3, Z4 or Z5;
- (z) at position 131 the amino acid residue is Z3, Z5 or Z6;
- (aa) at positions 125 and/or 128 the amino acid residue is Z4, Z5 or Z6;
- 10 (ab) at position 67 the amino acid residue is Z1, Z3, Z4 or Z5;
- (ac) at position 60 the amino acid residue is Z1, Z4, Z5 or Z6; and
- (ad) at position 37 the amino acid residue is Z3, Z4, Z5 or Z6;

wherein Z1 is an amino acid selected from the group consisting of A, I, L, M, and V; Z2 is an amino acid selected from the group consisting of F, W, and Y; Z3 is an amino acid selected from the group consisting of N, Q, S, and T; Z4 is an amino acid selected from the group consisting of R, H, and K; Z5 is an amino acid selected from the group consisting of D and E; and Z6 is an amino acid selected from the group consisting of C, G, and P.

108. The isolated or recombinant polynucleotide of claim 102, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 80% conform to the following restrictions:

- (a) at position 9, 76, 94 and 110 the amino acid residue is A;
- (b) at position 29 and 108 the amino acid residue is C;
- (c) at position 34 the amino acid residue is D;
- 25 (d) at position 95 the amino acid residue is E;
- (e) at position 56 the amino acid residue is F;
- (f) at position 43, 44, 66, 74, 87, 102, 116, 122, 127 and 136 the amino acid residue is G;
- (g) at position 41 the amino acid residue is H;
- (h) at position 7 the amino acid residue is I;
- 30 (i) at position 85 the amino acid residue is K;
- (j) at position 20, 36, 42, 50, 72, 78, 98 and 121 the amino acid residue is L;
- (k) at position 1, 75 and 141 the amino acid residue is M;
- (l) at position 23, 64 and 109 the amino acid residue is N;
- (m) at position 22, 25, 133, 134 and 137 the amino acid residue is P;

- (n) at position 71 the amino acid residue is Q;
- (o) at position 16, 21, 73, 99 and 111 the amino acid residue is R;
- (p) at position 55 and 88 the amino acid residue is S;
- (q) at position 77 the amino acid residue is T;
- 5 (r) at position 107 the amino acid residue is W; and
- (s) at position 13, 46, 70, 117 and 118 the amino acid residue is Y.

109. The isolated or recombinant polynucleotide of claim 1, wherein the amino acid residue in the amino acid sequence that correspond to position 28 is V.

- 110. The isolated or recombinant polynucleotide of claim 1, wherein the
10 amino acid sequence is selected from the group consisting of SEQ ID NOS:6-10 and 263-514.

111. The isolated or recombinant polypeptide of claim 42, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

- 15 (a) at positions 2, 4, 15, 19, 26, 28, 31, 45, 51, 54, 86, 90, 91, 97, 103, 105, 106, 114, 123, 129, 139, and/or 145 the amino acid residue is B1; and
- (b) at positions 3, 5, 8, 10, 11, 14, 17, 18, 24, 27, 32, 37, 38, 47, 48, 49, 52, 57, 58, 61, 62, 63, 68, 69, 79, 80, 82, 83, 89, 92, 100, 101, 104, 119, 120, 124, 125, 126, 128, 131, 143, and/or 144 the amino acid residue is B2;
- 20 wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y, and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

112. The isolated or recombinant polypeptide of claim 42, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions,
25 at least 80% conform to the following restrictions:

- (a) at positions 2, 4, 15, 19, 26, 28, 51, 54, 86, 90, 91, 97, 103, 105, 106, 114, 129, 139, and/or 145 the amino acid residue is Z1;
- (b) at positions 31 and/or 45 the amino acid residue is Z2;
- (c) at positions 8 and/or 89 the amino acid residue is Z3;
- 30 (d) at positions 82, 92, 101 and/or 120 the amino acid residue is Z4;
- (e) at positions 3, 11, 27 and/or 79 the amino acid residue is Z5;
- (f) at position 123 the amino acid residue is Z1 or Z2;
- (g) at positions 12, 33, 35, 39, 53, 59, 112, 132, 135, 140, and/or 146 the amino acid residue is Z1 or Z3;

- (h) at position 30 the amino acid residue is Z1 or Z4;
- (i) at position 6 the amino acid residue is Z1 or Z6;
- (j) at positions 81 and/or 113 the amino acid residue is Z2 or Z3;
- (k) at positions 138 and/or 142 the amino acid residue is Z2 or Z4;
- 5 (l) at positions 5, 17, 24, 57, 61, 124 and/or 126 the amino acid residue is Z3 or Z4;
- (m) at position 104 the amino acid residue is Z3 or Z5;
- (o) at positions 38, 52, 62 and/or 69 the amino acid residue is Z3 or Z6;
- (p) at positions 14, 119 and/or 144 the amino acid residue is Z4 or Z5;
- (q) at position 18 the amino acid residue is Z4 or Z6;
- 10 (r) at positions 10, 32, 48, 63, 80 and/or 83 the amino acid residue is Z5 or Z6;
- (s) at position 40 the amino acid residue is Z1, Z2 or Z3;
- (t) at positions 65 and/or 96 the amino acid residue is Z1, Z3 or Z5;
- (u) at positions 84 and/or 115 the amino acid residue is Z1, Z3 or Z4;
- (v) at position 93 the amino acid residue is Z2, Z3 or Z4;
- 15 (w) at position 130 the amino acid residue is Z2, Z4 or Z6;
- (x) at positions 47 and/or 58 the amino acid residue is Z3, Z4 or Z6;
- (y) at positions 49, 68, 100 and/or 143 the amino acid residue is Z3, Z4 or Z5;
- (z) at position 131 the amino acid residue is Z3, Z5 or Z6;
- (aa) at positions 125 and/or 128 the amino acid residue is Z4, Z5 or Z6;
- 20 (ab) at position 67 the amino acid residue is Z1, Z3, Z4 or Z5;
- (ac) at position 60 the amino acid residue is Z1, Z4, Z5 or Z6; and
- (ad) at position 37 the amino acid residue is Z3, Z4, Z5 or Z6;

wherein Z1 is an amino acid selected from the group consisting of A, I, L, M, and V; Z2 is an amino acid selected from the group consisting of F, W, and Y; Z3 is an amino acid selected from the group consisting of N, Q, S, and T; Z4 is an amino acid selected from the group consisting of R, H, and K; Z5 is an amino acid selected from the group consisting of D and E; and Z6 is an amino acid selected from the group consisting of C, G, and P.

- 113. The isolated or recombinant polypeptide of claim 42, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

- (a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110, 117, 118, 121, and/or 141 the amino acid residue is B1; and

(b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95, 99,

102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2; wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y,

5 and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

114. The isolated or recombinant polypeptide of claim 42, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

10 (a) at positions 1, 7, 9, 20, 36, 42, 50, 64, 72, 75, 76, 78, 94, 98, 110, 121, and/or 141 the amino acid residue is Z1;

(b) at positions 13, 46, 56, 70, 107, 117, and/or 118 the amino acid residue is Z2;

(c) at positions 23, 55, 71, 77, 88, and/or 109 the amino acid residue is Z3;

(d) at positions 16, 21, 41, 73, 85, 99, and/or 111 the amino acid residue is Z4;

15 (e) at positions 34 and/or 95 the amino acid residue is Z5;

(f) at position 22, 25, 29, 43, 44, 66, 74, 87, 102, 108, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is Z6;

wherein Z1 is an amino acid selected from the group consisting of A, I, L, M, and V; Z2 is an amino acid selected from the group consisting of F, W, and Y; Z3 is an amino acid selected from the group consisting of N, Q, S, and T; Z4 is an amino acid selected from the group consisting of R, H, and K; Z5 is an amino acid selected from the group consisting of D and E; and Z6 is an amino acid selected from the group consisting of C, G, and P.

25 115. The isolated or recombinant polypeptide of claim 111, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

(a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110, 117,

118, 121, and/or 141 the amino acid residue is B1; and

30 (b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95, 99,

102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2;

wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y, and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

116. The isolated or recombinant polypeptide of claim 111, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

(a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110, 117, 118, 121, and/or 141 the amino acid residue is B1; and

(b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95, 99,

102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2; wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y,

and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

117. The isolated or recombinant polypeptide of claim 111, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

(a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110, 117, 118, 121, and/or 141 the amino acid residue is B1; and

(b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95, 99,

102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2;

wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y, and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

118. The isolated or recombinant polypeptide of claim 112, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

(a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110, 117,

118, 121, and/or 141 the amino acid residue is B1; and

(b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95, 99,

102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2;

wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y,

5 and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

119. The isolated or recombinant polypeptide of claim 42, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 80% conform to the following restrictions:

- 10 (a) at position 2 the amino acid residue is I or L;
(b) at position 3 the amino acid residue is E or D;
(c) at position 4 the amino acid residue is V, A or I;
(d) at position 5 the amino acid residue is K, R or N;
(e) at position 6 the amino acid residue is P or L;
- 15 (f) at position 8 the amino acid residue is N, S or T;
(g) at position 10 the amino acid residue is E or G;
(h) at position 11 the amino acid residue is D or E;
(i) at position 12 the amino acid residue is T or A;
(j) at position 14 the amino acid residue is E or K;
- 20 (k) at position 15 the amino acid residue is I or L;
(l) at position 17 the amino acid residue is H or Q;
(m) at position 18 the amino acid residue is R, C or K;
(n) at position 19 the amino acid residue is I or V;
(o) at position 24 the amino acid residue is Q or R;
- 25 (p) at position 26 the amino acid residue is L or I;
(q) at position 27 the amino acid residue is E or D;
(r) at position 28 the amino acid residue is A or V;
(s) at position 30 the amino acid residue is K, M or R;
(t) at position 31 the amino acid residue is Y or F;
- 30 (u) at position 32 the amino acid residue is E or G;
(v) at position 33 the amino acid residue is T, A or S;
(w) at position 35 the amino acid residue is L, S or M;
(x) at position 37 the amino acid residue is R, G, E or Q;
(y) at position 38 the amino acid residue is G or S;

- (z) at position 39 the amino acid residue is T, A or S;
(aa) at position 40 the amino acid residue is F, L or S;
(ab) at position 45 the amino acid residue is Y or F;
(ac) at position 47 the amino acid residue is R, Q or G;
5 (ad) at position 48 the amino acid residue is G or D;
(ae) at position 49 the amino acid residue is K, R, E or Q;
(af) at position 51 the amino acid residue is I or V;
(ag) at position 52 the amino acid residue is S, C or G;
(ah) at position 53 the amino acid residue is I or T;
10 (ai) at position 54 the amino acid residue is A or V;
(aj) at position 57 the amino acid residue is H or N;
(ak) at position 58 the amino acid residue is Q, K, N or P;
(al) at position 59 the amino acid residue is A or S;
(am) at position 60 the amino acid residue is E, K, G, V or D;
15 (an) at position 61 the amino acid residue is H or Q;
(ao) at position 62 the amino acid residue is P, S or T;
(ap) at position 63 the amino acid residue is E, G or D;
(aq) at position 65 the amino acid residue is E, D, V or Q;
(ar) at position 67 the amino acid residue is Q, E, R, L, H or K;
20 (as) at position 68 the amino acid residue is K, R, E, or N;
(at) at position 69 the amino acid residue is Q or P;
(au) at position 79 the amino acid residue is E or D;
(av) at position 80 the amino acid residue is G or E;
(aw) at position 81 the amino acid residue is Y, N or F;
25 (ax) at position 82 the amino acid residue is R or H;
(ay) at position 83 the amino acid residue is E, G or D;
(az) at position 84 the amino acid residue is Q, R or L;
(ba) at position 86 the amino acid residue is A or V;
(bb) at position 89 the amino acid residue is T or S;
30 (bc) at position 90 the amino acid residue is L or I;
(bd) at position 91 the amino acid residue is I or V;
(be) at position 92 the amino acid residue is R or K;
(bf) at position 93 the amino acid residue is H, Y or Q;
(bg) at position 96 the amino acid residue is E, A or Q;

- (bh) at position 97 the amino acid residue is L or I;
- (bi) at position 100 the amino acid residue is K, R, N or E;
- (bj) at position 101 the amino acid residue is K or R;
- (bk) at position 103 the amino acid residue is A or V;
- 5 (bl) at position 104 the amino acid residue is D or N;
- (bm) at position 105 the amino acid residue is L or M;
- (bn) at position 106 the amino acid residue is L or I;
- (bo) at position 112 the amino acid residue is T or I;
- (bp) at position 113 the amino acid residue is S, T or F;
- 10 (bq) at position 114 the amino acid residue is A or V;
- (br) at position 115 the amino acid residue is S, R or A;
- (bs) at position 119 the amino acid residue is K, E or R;
- (bt) at position 120 the amino acid residue is K or R;
- (bu) at position 123 the amino acid residue is F or L;
- 15 (bv) at position 124 the amino acid residue is S or R;
- (bw) at position 125 the amino acid residue is E, K, G or D;
- (bx) at position 126 the amino acid residue is Q or H;
- (by) at position 128 the amino acid residue is E, G or K;
- (bz) at position 129 the amino acid residue is V, I or A;
- 20 (ca) at position 130 the amino acid residue is Y, H, F or C;
- (cb) at position 131 the amino acid residue is D, G, N or E;
- (cc) at position 132 the amino acid residue is I, T, A, M, V or L;
- (cd) at position 135 the amino acid residue is V, T, A or I;
- (ce) at position 138 the amino acid residue is H or Y;
- 25 (cf) at position 139 the amino acid residue is I or V;
- (cg) at position 140 the amino acid residue is L or S;
- (ch) at position 142 the amino acid residue is Y or H;
- (ci) at position 143 the amino acid residue is K, T or E;
- (cj) at position 144 the amino acid residue is K, E or R;
- 30 (ck) at position 145 the amino acid residue is L or I; and
- (cl) at position 146 the amino acid residue is T or A.

120. The isolated or recombinant polypeptide of claim 42, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 80% conform to the following restrictions:

- (a) at position 9, 76, 94 and 110 the amino acid residue is A;
- (b) at position 29 and 108 the amino acid residue is C;
- (c) at position 34 the amino acid residue is D;
- (d) at position 95 the amino acid residue is E;
- 5 (e) at position 56 the amino acid residue is F;
- (f) at position 43, 44, 66, 74, 87, 102, 116, 122, 127 and 136 the amino acid residue is G;
- (g) at position 41 the amino acid residue is H;
- (h) at position 7 the amino acid residue is I;
- (i) at position 85 the amino acid residue is K;
- 10 (j) at position 20, 36, 42, 50, 72, 78, 98 and 121 the amino acid residue is L;
- (k) at position 1, 75 and 141 the amino acid residue is M;
- (l) at position 23, 64 and 109 the amino acid residue is N;
- (m) at position 22, 25, 133, 134 and 137 the amino acid residue is P;
- (n) at position 71 the amino acid residue is Q;
- 15 (o) at position 16, 21, 73, 99 and 111 the amino acid residue is R;
- (p) at position 55 and 88 the amino acid residue is S;
- (q) at position 77 the amino acid residue is T;
- (r) at position 107 the amino acid residue is W; and
- (s) at position 13, 46, 70, 117 and 118 the amino acid residue is Y.

20 121. The isolated or recombinant polypeptide of claim 119, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

- (a) at positions 1, 7, 9, 13, 20, 36, 42, 46, 50, 56, 64, 70, 72, 75, 76, 78, 94, 98, 107, 110, 117,
- 25 118, 121, and/or 141 the amino acid residue is B1; and
- (b) at positions 16, 21, 22, 23, 25, 29, 34, 41, 43, 44, 55, 66, 71, 73, 74, 77, 85, 87, 88, 95, 99,
- 102, 108, 109, 111, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is B2;
- wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y,
- 30 and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

122. The isolated or recombinant polypeptide of claim 120, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

(a) at positions 2, 4, 15, 19, 26, 28, 31, 45, 51, 54, 86, 90, 91, 97, 103, 105, 106, 114, 123, 129, 139, and/or 145 the amino acid residue is B1; and

(b) at positions 3, 5, 8, 10, 11, 14, 17, 18, 24, 27, 32, 37, 38, 47, 48, 49, 52, 57, 58, 61, 62, 63, 68, 69, 79, 80, 82, 83, 89, 92, 100, 101, 104, 119, 120, 124, 125, 126, 128, 131,

5 143, and/or 144 the amino acid residue is B2;

wherein B1 is an amino acid selected from the group consisting of A, I, L, M, F, W, Y, and V; and B2 is an amino acid selected from the group consisting of R, N, D, C, Q, E, G, H, K, P, S, and T.

10 123. The isolated or recombinant polypeptide of claim 119, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 90% conform to the following restrictions:

(a) at positions 1, 7, 9, 20, 36, 42, 50, 64, 72, 75, 76, 78, 94, 98, 110, 121, and/or 141 the amino acid residue is Z1;

(b) at positions 13, 46, 56, 70, 107, 117, and/or 118 the amino acid residue is Z2;

15 (c) at positions 23, 55, 71, 77, 88, and/or 109 the amino acid residue is Z3;

(d) at positions 16, 21, 41, 73, 85, 99, and/or 111 the amino acid residue is Z4;

(e) at positions 34 and/or 95 the amino acid residue is Z5;

(f) at position 22, 25, 29, 43, 44, 66, 74, 87, 102, 108, 116, 122, 127, 133, 134, 136, and/or 137 the amino acid residue is Z6;

20 wherein Z1 is an amino acid selected from the group consisting of A, I, L, M, and V; Z2 is an amino acid selected from the group consisting of F, W, and Y; Z3 is an amino acid selected from the group consisting of N, Q, S, and T; Z4 is an amino acid selected from the group consisting of R, H, and K; Z5 is an amino acid selected from the group consisting of D and E; and Z6 is an amino acid selected from the group consisting of
25 C, G, and P.

124. The isolated or recombinant polypeptide of claim 120, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 80% conform to the following restrictions:

30 (a) at positions 2, 4, 15, 19, 26, 28, 51, 54, 86, 90, 91, 97, 103, 105, 106, 114, 129, 139, and/or 145 the amino acid residue is Z1;

(b) at positions 31 and/or 45 the amino acid residue is Z2;

(c) at positions 8 and/or 89 the amino acid residue is Z3;

(d) at positions 82, 92, 101 and/or 120 the amino acid residue is Z4;

(e) at positions 3, 11, 27 and/or 79 the amino acid residue is Z5;

- (f) at position 123 the amino acid residue is Z1 or Z2;
- (g) at positions 12, 33, 35, 39, 53, 59, 112, 132, 135, 140, and/or 146 the amino acid residue is Z1 or Z3;
- (h) at position 30 the amino acid residue is Z1 or Z4;
- 5 (i) at position 6 the amino acid residue is Z1 or Z6;
- (j) at positions 81 and/or 113 the amino acid residue is Z2 or Z3;
- (k) at positions 138 and/or 142 the amino acid residue is Z2 or Z4;
- (l) at positions 5, 17, 24, 57, 61, 124 and/or 126 the amino acid residue is Z3 or Z4;
- (m) at position 104 the amino acid residue is Z3 or Z5;
- 10 (o) at positions 38, 52, 62 and/or 69 the amino acid residue is Z3 or Z6;
- (p) at positions 14, 119 and/or 144 the amino acid residue is Z4 or Z5;
- (q) at position 18 the amino acid residue is Z4 or Z6;
- (r) at positions 10, 32, 48, 63, 80 and/or 83 the amino acid residue is Z5 or Z6;
- (s) at position 40 the amino acid residue is Z1, Z2 or Z3;
- 15 (t) at positions 65 and/or 96 the amino acid residue is Z1, Z3 or Z5;
- (u) at positions 84 and/or 115 the amino acid residue is Z1, Z3 or Z4;
- (v) at position 93 the amino acid residue is Z2, Z3 or Z4;
- (w) at position 130 the amino acid residue is Z2, Z4 or Z6;
- (x) at positions 47 and/or 58 the amino acid residue is Z3, Z4 or Z6;
- 20 (y) at positions 49, 68, 100 and/or 143 the amino acid residue is Z3, Z4 or Z5;
- (z) at position 131 the amino acid residue is Z3, Z5 or Z6;
- (aa) at positions 125 and/or 128 the amino acid residue is Z4, Z5 or Z6;
- (ab) at position 67 the amino acid residue is Z1, Z3, Z4 or Z5;
- (ac) at position 60 the amino acid residue is Z1, Z4, Z5 or Z6; and
- 25 (ad) at position 37 the amino acid residue is Z3, Z4, Z5 or Z6;
- wherein Z1 is an amino acid selected from the group consisting of A, I, L, M, and V; Z2 is an amino acid selected from the group consisting of F, W, and Y; Z3 is an amino acid selected from the group consisting of N, Q, S, and T; Z4 is an amino acid selected from the group consisting of R, H, and K; Z5 is an amino acid selected from the group consisting of D and E; and Z6 is an amino acid selected from the group consisting of C, G, and P.
- 30

125. The isolated or recombinant polypeptide of claim 119, wherein of the amino acid residues in the amino acid sequence that correspond to the following positions, at least 80% conform to the following restrictions:

- (a) at position 9, 76, 94 and 110 the amino acid residue is A;
- (b) at position 29 and 108 the amino acid residue is C;
- (c) at position 34 the amino acid residue is D;
- (d) at position 95 the amino acid residue is E;
- 5 (e) at position 56 the amino acid residue is F;
- (f) at position 43, 44, 66, 74, 87, 102, 116, 122, 127 and 136 the amino acid residue is G;
- (g) at position 41 the amino acid residue is H;
- (h) at position 7 the amino acid residue is I;
- (i) at position 85 the amino acid residue is K;
- 10 (j) at position 20, 36, 42, 50, 72, 78, 98 and 121 the amino acid residue is L;
- (k) at position 1, 75 and 141 the amino acid residue is M;
- (l) at position 23, 64 and 109 the amino acid residue is N;
- (m) at position 22, 25, 133, 134 and 137 the amino acid residue is P;
- (n) at position 71 the amino acid residue is Q;
- 15 (o) at position 16, 21, 73, 99 and 111 the amino acid residue is R;
- (p) at position 55 and 88 the amino acid residue is S;
- (q) at position 77 the amino acid residue is T;
- (r) at position 107 the amino acid residue is W; and
- (s) at position 13, 46, 70, 117 and 118 the amino acid residue is Y.

20 126. The isolated or recombinant polypeptide of claim 24, wherein the amino acid residue in the amino acid sequence that correspond to position 28 is V.

127. The isolated or recombinant polypeptide of claim 42, wherein the amino acid sequence is selected from the group consisting of SEQ ID NOS:6-10 and 263-514.

25 128. A transgenic plant or transgenic plant explant having an enhanced tolerance to glyphosate, wherein the plant or plant explant expresses a polypeptide with glyphosate N-acetyltransferase activity and at least one polypeptide imparting glyphosate tolerance by an additional mechanism.

30 129. The transgenic plant or transgenic plant explant of claim 128, wherein the polypeptide with glyphosate N-acetyltransferase activity comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 6-10 and 263-514.

130. The transgenic plant or transgenic plant explant of claim 129, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is selected from the group consisting of a glyphosate-tolerant 5-

enolpyruvylshikimate-3-phosphate synthase and a glyphosate-tolerant glyphosate oxido-reductase.

131. The transgenic plant or transgenic plant explant of claim 130, wherein the at least one polypeptide imparting glyphosate tolerance by an additional
5 mechanism is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase.

132. The transgenic plant or transgenic plant explant of claim 130, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant glyphosate oxido-reductase.

133. A transgenic plant or transgenic plant explant, wherein the plant or
10 plant explant expresses a polypeptide with glyphosate N-acetyltransferase activity and at least one polypeptide imparting tolerance to an additional herbicide.

134. The transgenic plant or transgenic plant explant of claim 133, wherein the polypeptide with glyphosate N-acetyltransferase activity comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 6-10 and 263-514.

135. The transgenic plant or transgenic plant explant of claim 134,
15 wherein the at least one polypeptide imparting tolerance to an additional herbicide is selected from the group consisting of a mutated hydroxyphenylpyruvatedioxygenase, a sulfonamide-tolerant acetolactate synthase, a sulfonamide-tolerant acetohydroxy acid synthase, an imidazolinone-tolerant acetolactate synthase, an imidazolinone-tolerant
20 acetohydroxy acid synthase, a phosphinothricin acetyl transferase and a mutated protoporphyrinogen oxidase.

136. The transgenic plant or transgenic plant explant of claim 135, wherein the at least one polypeptide imparting tolerance to an additional herbicide is a mutated hydroxyphenylpyruvatedioxygenase.

137. The transgenic plant or transgenic plant explant of claim 135,
25 wherein the at least one polypeptide imparting tolerance to an additional herbicide is a sulfonamide-tolerant acetolactate synthase.

138. The transgenic plant or transgenic plant explant of claim 135, wherein the at least one polypeptide imparting tolerance to an additional herbicide is a
30 sulfonamide-tolerant acetohydroxy acid synthase.

139. The transgenic plant or transgenic plant explant of claim 135, wherein the at least one polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetolactate synthase.

140. The transgenic plant or transgenic plant explant of claim 135, wherein the at least one polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetohydroxy acid synthase.

141. The transgenic plant or transgenic plant explant of claim 135, wherein the at least one polypeptide imparting tolerance to an additional herbicide is a phosphinothricin acetyl transferase.

142. The transgenic plant or transgenic plant explant of claim 135, wherein the at least one polypeptide imparting tolerance to an additional herbicide is a mutated protoporphyrinogen oxidase.

143. A transgenic plant or transgenic plant explant having an enhanced tolerance to glyphosate, wherein the plant or plant explant expresses a polypeptide with glyphosate N-acetyltransferase activity, at least one polypeptide imparting glyphosate tolerance by an additional mechanism, and at least one polypeptide imparting tolerance to an additional herbicide.

144. The transgenic plant or transgenic plant explant of claim 143, wherein the polypeptide with glyphosate N-acetyltransferase activity comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 6-10 and 263-514.

145. The transgenic plant or transgenic plant explant of claim 144, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is selected from the group consisting of a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and a glyphosate-tolerant glyphosate oxidoreductase and the at least one polypeptide imparting tolerance to an additional herbicide is selected from the group consisting of a mutated hydroxyphenylpyruvatedioxygenase, a sulfonamide-tolerant acetolactate synthase, a sulfonamide-tolerant acetohydroxy acid synthase, an imidazolinone-tolerant acetolactate synthase, an imidazolinone-tolerant acetohydroxy acid synthase, a phosphinothricin acetyl transferase and a mutated protoporphyrinogen oxidase.

146. The transgenic plant or transgenic plant explant of claim 145, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the at least one polypeptide imparting tolerance to an additional herbicide is a mutated hydroxyphenylpyruvatedioxygenase.

147. The transgenic plant or transgenic plant explant of claim 145, wherein the at least one polypeptide imparting glyphosate tolerance by an additional

mechanism is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the at least one polypeptide imparting tolerance to an additional herbicide is a sulfonamide-tolerant acetolactate synthase.

148. The transgenic plant or transgenic plant explant of claim 145,
5 wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the at least one polypeptide imparting tolerance to an additional herbicide is a sulfonamide-tolerant acetohydroxy acid synthase.

149. The transgenic plant or transgenic plant explant of claim 145,
10 wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the at least one polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetolactate synthase.

150. The transgenic plant or transgenic plant explant of claim 145,
15 wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the at least one polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetohydroxy acid synthase.

151. The transgenic plant or transgenic plant explant of claim 145,
20 wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the at least one polypeptide imparting tolerance to an additional herbicide is a phosphinothricin acetyl transferase.

152. The transgenic plant or transgenic plant explant of claim 145,
25 wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the at least one polypeptide imparting tolerance to an additional herbicide is a mutated protoporphyrinogen oxidase.

153. The transgenic plant or transgenic plant explant of claim 145,
30 wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant glyphosate oxido-reductase and the at least one polypeptide imparting tolerance to an additional herbicide is a mutated hydroxyphenylpyruvatedioxygenase.

154. The transgenic plant or transgenic plant explant of claim 145, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant glyphosate oxido-reductase and the at least one polypeptide imparting tolerance to an additional herbicide is a sulfonamide-tolerant acetolactate synthase.

155. The transgenic plant or transgenic plant explant of claim 145, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant glyphosate oxido-reductase and the at least one polypeptide imparting tolerance to an additional herbicide is a sulfonamide-tolerant acetohydroxy acid synthase.

156. The transgenic plant or transgenic plant explant of claim 145, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant glyphosate oxido-reductase and the at least one polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetolactate synthase.

157. The transgenic plant or transgenic plant explant of claim 145, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant glyphosate oxido-reductase and the at least one polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetohydroxy acid synthase.

158. The transgenic plant or transgenic plant explant of claim 145, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant glyphosate oxido-reductase and the at least one polypeptide imparting tolerance to an additional herbicide is a phosphinothricin acetyl transferase.

159. The transgenic plant or transgenic plant explant of claim 145, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant glyphosate oxido-reductase and the at least one polypeptide imparting tolerance to an additional herbicide is a mutated protoporphyrinogen oxidase.

160. A transgenic plant or transgenic plant explant having an enhanced tolerance to glyphosate, wherein the plant or plant explant expresses a polypeptide with glyphosate N-acetyltransferase activity and at least one of a polypeptide selected from the

group consisting of a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and a glyphosate-tolerant glyphosate oxido-reductase.

161. The transgenic plant or transgenic plant explant of claim 160, wherein the polypeptide with glyphosate N-acetyltransferase activity comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 6-10 and 263-514.

162. The transgenic plant or transgenic plant explant of claim 161, wherein the at least one polypeptide is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase.

163. The transgenic plant or transgenic plant explant of claim 161, wherein the at least one polypeptide is a glyphosate-tolerant glyphosate oxido-reductase.

164. A transgenic plant or transgenic plant explant, wherein the plant or plant explant expresses a polypeptide with glyphosate N-acetyltransferase activity and at least one polypeptide selected from the group consisting of a mutated hydroxyphenylpyruvatedioxygenase, a sulfonamide-tolerant acetolactate synthase, a sulfonamide-tolerant acetohydroxy acid synthase, an imidazolinone-tolerant acetolactate synthase, an imidazolinone-tolerant acetohydroxy acid synthase, a phosphinothricin acetyl transferase and a mutated protoporphyrinogen oxidase.

165. The transgenic plant or transgenic plant explant of claim 164, wherein the polypeptide with glyphosate N-acetyltransferase activity comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 6-10 and 263-514.

166. The transgenic plant or transgenic plant explant of claim 165, wherein the at least one polypeptide is a mutated hydroxyphenylpyruvatedioxygenase.

167. The transgenic plant or transgenic plant explant of claim 165, wherein the at least one polypeptide is a sulfonamide-tolerant acetolactate synthase.

168. The transgenic plant or transgenic plant explant of claim 165, wherein the at least one polypeptide is a sulfonamide-tolerant acetohydroxy acid synthase.

169. The transgenic plant or transgenic plant explant of claim 165, wherein the at least one polypeptide is an imidazolinone-tolerant acetolactate synthase.

170. The transgenic plant or transgenic plant explant of claim 165, wherein the at least one polypeptide is an imidazolinone-tolerant acetohydroxy acid synthase.

171. The transgenic plant or transgenic plant explant of claim 165, wherein the at least one polypeptide is a phosphinothricin acetyl transferase.

172. The transgenic plant or transgenic plant explant of claim 165, wherein the at least one polypeptide is a mutated protoporphyrinogen oxidase.

173. A transgenic plant or transgenic plant explant having an enhanced tolerance to glyphosate, wherein the plant or plant explant expresses a polypeptide with
5 glyphosate N-acetyltransferase activity, at least one of a first polypeptide selected from the group consisting of a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and a glyphosate-tolerant glyphosate oxido-reductase and at least one of a second polypeptide selected from the group consisting of a mutated hydroxyphenylpyruvatedioxygenase, a sulfonamide-tolerant acetolactate synthase, a
10 sulfonamide-tolerant acetohydroxy acid synthase, an imidazolinone-tolerant acetolactate synthase, an imidazolinone-tolerant acetohydroxy acid synthase, a phosphinothricin acetyl transferase and a mutated protoporphyrinogen oxidase.

174. The transgenic plant or transgenic plant explant of claim 173, wherein the polypeptide with glyphosate N-acetyltransferase activity comprises an amino
15 acid sequence selected from the group consisting of SEQ ID NOS: 6-10 and 263-514.

175. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the second polypeptide is a mutated hydroxyphenylpyruvatedioxygenase.

176. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate
20 synthase and the second polypeptide is a sulfonamide-tolerant acetolactate synthase.

177. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the second polypeptide is a sulfonamide-tolerant acetohydroxy acid synthase.
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178. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the second polypeptide is an imidazolinone-tolerant acetolactate synthase.

179. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate
30 synthase and the second polypeptide is an imidazolinone-tolerant acetohydroxy acid synthase.

180. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the second polypeptide is a phosphinothricin acetyl transferase.

181. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and the second polypeptide is a mutated protoporphyrinogen oxidase.

182. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant glyphosate oxido-reductase and the second polypeptide is a mutated hydroxyphenylpyruvatedioxygenase.

183. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant glyphosate oxido-reductase and the second polypeptide is a sulfonamide-tolerant acetolactate synthase.

184. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant glyphosate oxido-reductase and the second polypeptide is a sulfonamide-tolerant acetohydroxy acid synthase.

185. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant glyphosate oxido-reductase and the second polypeptide is an imidazolinone-tolerant acetolactate synthase.

186. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant glyphosate oxido-reductase and the second polypeptide is an imidazolinone-tolerant acetohydroxy acid synthase.

187. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant glyphosate oxido-reductase and the second polypeptide is a phosphinothricin acetyl transferase.

188. The transgenic plant or transgenic plant explant of claim 174, wherein the first polypeptide is a glyphosate-tolerant glyphosate oxido-reductase and the second polypeptide is a mutated protoporphyrinogen oxidase.

189. A transgenic plant or transgenic plant explant having an enhanced tolerance to glyphosate, wherein the plant or plant explant expresses a polypeptide with glyphosate N-acetyltransferase activity and at least one polypeptide selected from the group consisting of a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase, a glyphosate-tolerant glyphosate oxido-reductase, a mutated hydroxyphenylpyruvatedioxygenase, a sulfonamide-tolerant acetolactate synthase, a sulfonamide-tolerant acetohydroxy acid synthase, an imidazolinone-tolerant acetolactate synthase, an imidazolinone-tolerant acetohydroxy acid synthase, a phosphinothricin acetyl transferase and a mutated protoporphyrinogen oxidase.

190. The transgenic plant or transgenic plant explant of claim 189, wherein the polypeptide with glyphosate N-acetyltransferase activity comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 6-10 and 263-514.

191. The transgenic plant or transgenic plant explant of claim 190,
5 wherein the polypeptide is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase.

192. The transgenic plant or transgenic plant explant of claim 190, wherein the polypeptide is a glyphosate-tolerant glyphosate oxido-reductase.

193. The transgenic plant or transgenic plant explant of claim 190,
10 wherein the polypeptide is a mutated hydroxyphenylpyruvatedioxygenase.

194. The transgenic plant or transgenic plant explant of claim 190, wherein the polypeptide is a sulfonamide-tolerant acetolactate synthase.

195. The transgenic plant or transgenic plant explant of claim 190, wherein the polypeptide is a sulfonamide-tolerant acetohydroxy acid synthase.

196. The transgenic plant or transgenic plant explant of claim 190,
15 wherein the polypeptide is an imidazolinone-tolerant acetolactate synthase.

197. The transgenic plant or transgenic plant explant of claim 190, wherein the polypeptide is an imidazolinone-tolerant acetohydroxy acid synthase.

198. The transgenic plant or transgenic plant explant of claim 190,
20 wherein the polypeptide is a phosphinothricin acetyl transferase.

199. The transgenic plant or transgenic plant explant of claim 190, wherein the polypeptide is a mutated protoporphyrinogen oxidase.

200. A method for controlling weeds in a field containing a crop comprising:

- 25 (a) planting the field with crop seeds or plants which are transformed with a gene encoding a glyphosate N-acetyltransferase and at least one gene encoding a polypeptide imparting glyphosate tolerance by an additional mechanism; and
(b) applying to the crop and weeds in the field an effective application of glyphosate sufficient to inhibit growth of the weeds in the field without significantly affecting the
30 crop.

201. The method of claim 200, wherein the gene encoding a glyphosate N-acetyltransferase comprises a polynucleotide sequence selected from the group consisting of SEQ ID NOS: 1-5 and 11-262.

202. The method of claim 201, wherein the polypeptide imparting glyphosate tolerance by an additional mechanism is selected from the group consisting of a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and a glyphosate-tolerant glyphosate oxido-reductase.

203. The method of claim 202, wherein the polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase.

204. The method of claim 202, wherein the polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant glyphosate oxido-reductase.

205. A method for preventing emergence of glyphosate resistant weeds in a field containing a crop comprising:

- (a) planting the field with crop seeds or plants which are transformed with a gene encoding a glyphosate N-acetyltransferase and at least one gene encoding a polypeptide imparting glyphosate tolerance by an additional mechanism; and
- (b) applying to the crop and weeds in the field an effective application of glyphosate.

206. The method of claim 205, wherein the gene encoding a glyphosate N-acetyltransferase comprises a polynucleotide sequence selected from the group consisting of SEQ ID NOS: 1-5 and 11-262.

207. The method of claim 206, wherein the polypeptide imparting glyphosate tolerance by an additional mechanism is selected from the group consisting of a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and a glyphosate-tolerant glyphosate oxido-reductase.

208. The method of claim 207, wherein the polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase.

209. The method of claim 207, wherein the polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant glyphosate oxido-reductase.

210. A method for selectively controlling weeds in a field containing a crop comprising:

- (a) planting the field with crop seeds or plants which are transformed with a gene encoding a glyphosate N-acetyltransferase and at least one gene encoding a polypeptide imparting tolerance to an additional herbicide, and;

(b) applying to the crop and weeds in the field a simultaneous or chronologically staggered application of glyphosate and the additional herbicide which is sufficient to inhibit growth of the weeds in the field without significantly affecting the crop.

211. The method of claim 210, wherein the gene encoding a glyphosate
5 N-acetyltransferase comprises a polynucleotide sequence selected from the group consisting of SEQ ID NOS: 1-5 and 11-262.

212. The method of claim 211, wherein the at least one polypeptide
imparting tolerance to an additional herbicide is selected from the group consisting of a
mutated hydroxyphenylpyruvatedioxygenase, a sulfonamide-tolerant acetolactate
10 synthase, a sulfonamide-tolerant acetohydroxy acid synthase, an imidazolinone-tolerant
acetolactate synthase, an imidazolinone-tolerant acetohydroxy acid synthase, a
phosphinothricin acetyl transferase and a mutated protoporphyrinogen oxidase.

213. The method of claim 211, wherein the additional herbicide is
selected from the group consisting of a hydroxyphenylpyruvatedioxygenase inhibitor,
15 sulfonamide, imidazolinone, bialaphos, phosphinothricin, azafenidin, butafenacil,
sulfosate, glufosinate, and a protox inhibitor.

214. The method of claim 212, wherein the polypeptide imparting
tolerance to an additional herbicide is a mutated hydroxyphenylpyruvatedioxygenase.

215. The method of claim 212, wherein the polypeptide imparting
20 tolerance to an additional herbicide is a sulfonamide-tolerant acetolactate synthase.

216. The method of claim 212, wherein the polypeptide imparting
tolerance to an additional herbicide is a sulfonamide-tolerant acetohydroxy acid synthase.

217. The method of claim 212, wherein the polypeptide imparting
tolerance to an additional herbicide is an imidazolinone-tolerant acetolactate synthase.

218. The method of claim 212, wherein the polypeptide imparting
25 tolerance to an additional herbicide is an imidazolinone-tolerant acetohydroxy acid
synthase.

219. The method of claim 212, wherein the polypeptide imparting
tolerance to an additional herbicide is a phosphinothricin acetyl transferase.

220. The method of claim 212, wherein the polypeptide imparting
30 tolerance to an additional herbicide is a mutated protoporphyrinogen oxidase.

221. A method for preventing emergence of herbicide resistant weeds in
a field containing a crop comprising:

- (a) planting the field with crop seeds or plants which are transformed with a gene encoding a glyphosate N-acetyltransferase and at least one gene encoding a polypeptide imparting tolerance to an additional herbicide, and;
- (b) applying to the crop and weeds in the field a simultaneous or chronologically staggered application of glyphosate and the additional herbicide.

222. The method of claim 221, wherein the gene encoding a glyphosate N-acetyltransferase comprises a polynucleotide sequence selected from the group consisting of SEQ ID NOS: 1-5 and 11-262.

223. The method of claim 222, wherein the at least one polypeptide imparting tolerance to an additional herbicide is selected from the group consisting of a mutated hydroxyphenylpyruvatedioxygenase, a sulfonamide-tolerant acetolactate synthase, a sulfonamide-tolerant acetohydroxy acid synthase, an imidazolinone-tolerant acetolactate synthase, an imidazolinone-tolerant acetohydroxy acid synthase, a phosphinothricin acetyl transferase and a mutated protoporphyrinogen oxidase.

224. The method of claim 221, wherein the additional herbicide is selected from the group consisting of a hydroxyphenylpyruvatedioxygenase inhibitor, sulfonamide, imidazolinone, bialaphos, phosphinothricin, azafenidin, butafenacil, sulfosate, glufosinate, and a protox inhibitor.

225. The method of claim 223, wherein the polypeptide imparting tolerance to an additional herbicide is a mutated hydroxyphenylpyruvatedioxygenase.

226. The method of claim 223, wherein the polypeptide imparting tolerance to an additional herbicide is a sulfonamide-tolerant acetolactate synthase.

227. The method of claim 223, wherein the polypeptide imparting tolerance to an additional herbicide is a sulfonamide-tolerant acetohydroxy acid synthase.

228. The method of claim 223, wherein the polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetolactate synthase.

229. The method of claim 223, wherein the polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetohydroxy acid synthase.

230. The method of claim 223, wherein the polypeptide imparting tolerance to an additional herbicide is a phosphinothricin acetyl transferase.

231. The method of claim 223, wherein the polypeptide imparting tolerance to an additional herbicide is a mutated protoporphyrinogen oxidase.

232. A method for selectively controlling weeds in a field containing a crop comprising:

- (a) planting the field with crop seeds or plants which are transformed with a gene encoding a glyphosate N-acetyltransferase, at least one gene encoding a polypeptide imparting glyphosate tolerance by an additional mechanism and at least one gene encoding a polypeptide imparting tolerance to an additional herbicide, and;
- (b) applying to the crop and weeds in the field a simultaneous or chronologically staggered application of glyphosate and the additional herbicide which is sufficient to inhibit growth of the weeds in the field without significantly affecting the crop.

233. The method of claim 232, wherein the gene encoding a glyphosate N-acetyltransferase comprises a polynucleotide sequence selected from the group consisting of SEQ ID NOS: 1-5 and 11-262.

234. The transgenic plant or transgenic plant explant of claim 233, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is selected from the group consisting of a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase and a glyphosate-tolerant glyphosate oxidoreductase.

235. The transgenic plant or transgenic plant explant of claim 234, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthase.

236. The transgenic plant or transgenic plant explant of claim 234, wherein the at least one polypeptide imparting glyphosate tolerance by an additional mechanism is a glyphosate-tolerant glyphosate oxidoreductase.

237. The method of claim 233, wherein the at least one polypeptide imparting tolerance to an additional herbicide is selected from the group consisting of a mutated hydroxyphenylpyruvate dioxygenase, a sulfonamide-tolerant acetolactate synthase, a sulfonamide-tolerant acetohydroxy acid synthase, an imidazolinone-tolerant acetolactate synthase, an imidazolinone-tolerant acetohydroxy acid synthase, a phosphinothricin acetyl transferase and a mutated protoporphyrinogen oxidase.

238. The method of claim 233, wherein the additional herbicide is selected from the group consisting of a hydroxyphenylpyruvate dioxygenase inhibitor, sulfonamide, imidazolinone, bialaphos, phosphinothricin, azafenidin, butafenacil, sulfosate, glufosinate, and a protox inhibitor.

239. The method of claim 237, wherein the polypeptide imparting tolerance to an additional herbicide is a mutated hydroxyphenylpyruvatedioxygenase.

240. The method of claim 237, wherein the polypeptide imparting tolerance to an additional herbicide is a sulfonamide-tolerant acetolactate synthase.

241. The method of claim 237, wherein the polypeptide imparting tolerance to an additional herbicide is a sulfonamide-tolerant acetohydroxy acid synthase.

242. The method of claim 237, wherein the polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetolactate synthase.

243. The method of claim 237, wherein the polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetohydroxy acid synthase.

244. The method of claim 237, wherein the polypeptide imparting tolerance to an additional herbicide is a phosphinothricin acetyl transferase.

245. The method of claim 237, wherein the polypeptide imparting tolerance to an additional herbicide is a mutated protoporphyrinogen oxidase.

246. A method for preventing emergence of herbicide resistant weeds in a field containing a crop comprising:

(a) planting the field with crop seeds or plants which are transformed with a gene encoding a glyphosate N-acetyltransferase, at least one gene encoding a polypeptide imparting glyphosate tolerance by an additional mechanism and at least one gene encoding a polypeptide imparting tolerance to an additional herbicide, and;

(b) applying to the crop and weeds in the field a simultaneous or chronologically staggered application of glyphosate and the additional herbicide.

247. The method of claim 246, wherein the gene encoding a glyphosate N-acetyltransferase comprises a polynucleotide sequence selected from the group consisting of SEQ ID NOS: 1-5 and 11-262.

248. The method of claim 247, wherein the at least one polypeptide imparting tolerance to an additional herbicide is selected from the group consisting of a mutated hydroxyphenylpyruvatedioxygenase, a sulfonamide-tolerant acetolactate synthase, a sulfonamide-tolerant acetohydroxy acid synthase, an imidazolinone-tolerant acetolactate synthase, an imidazolinone-tolerant acetohydroxy acid synthase, a phosphinothricin acetyl transferase and a mutated protoporphyrinogen oxidase.

249. The method of claim 247, wherein the additional herbicide is selected from the group consisting of a hydroxyphenylpyruvatedioxygenase inhibitor,

sulfonamide, imidazolinone, bialaphos, phosphinothricin, azafenidin, butafenacil, sulfosate, glufosinate, and a protox inhibitor.

250. The method of claim 248, wherein the polypeptide imparting tolerance to an additional herbicide is a mutated hydroxyphenylpyruvatedioxygenase.

5 251. The method of claim 248, wherein the polypeptide imparting tolerance to an additional herbicide is a sulfonamide-tolerant acetolactate synthase.

252. The method of claim 248, wherein the polypeptide imparting tolerance to an additional herbicide is a sulfonamide-tolerant acetohydroxy acid synthase.

10 253. The method of claim 248, wherein the polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetolactate synthase.

254. The method of claim 248, wherein the polypeptide imparting tolerance to an additional herbicide is an imidazolinone-tolerant acetohydroxy acid synthase.

15 255. The method of claim 248, wherein the polypeptide imparting tolerance to an additional herbicide is a phosphinothricin acetyl transferase.

256. The method of claim 248, wherein the polypeptide imparting tolerance to an additional herbicide is a mutated protoporphyrinogen oxidase.